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## RAW SEQUENCE LISTING

DATE: 01/23/2002

PATENT APPLICATION: US/09/997,522

TIME: 10:04:02

Input Set : N:\Crf3\RULE60\09997522.raw.txt

Output Set: N:\CRF3\01232002\I997522.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Coleman, Roger

6 Au-Young, Janice

7 Bandman, Olga

8 Seilhamer, Jeffrey J.

10 (ii) TITLE OF INVENTION: Thrombin Receptor Homolog

12 (iii) NUMBER OF SEQUENCES: 2

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

16 (B) STREET: 3330 Hillview Avenue

17 (C) CITY: Palo Alto

18 (D) STATE: CA

19 (E) COUNTRY: USA

20 (F) ZIP: 94304

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

C--&gt; 29 (A) APPLICATION NUMBER: US/09/997,522

C--&gt; 30 (B) FILING DATE: 28-Nov-2001

31 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 08/467,125

35 (B) FILING DATE:

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: Luther, Barbara J.

41 (B) REGISTRATION NUMBER: 33954

42 (C) REFERENCE/DOCKET NUMBER: PF-0041 US

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: 415-855-0555

46 (B) TELEFAX: 415-852-0195

49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 1143 base pairs

53 (B) TYPE: nucleic acid

54 (C) STRANDEDNESS: single

55 (D) TOPOLOGY: linear

57 (ii) MOLECULE TYPE: cDNA

60 (vii) IMMEDIATE SOURCE:

61 (A) LIBRARY: Liver

ENTERED

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62          (B) CLONE: 86700
66      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
68 ATGAGAAGTC ATACCATAAC AATGACGACA ACTTCAGTCA GCAGCTGGCC TTACTCCTCC      60
70 CACAGAATGC GCTTTATAAC CAATCATAGC GACCAACCGC CACAAAACCT CTCAGCAACA      120
72 CCAAATGTTA CTACCTGTCC CATGGATGAA AAATTGCTAT CTACTGTGTT AACCACATCC      180
74 TACTCTGTTA TTTTCATCGT GGGACTGGTT GGAACATAA TCGCCCCCTA TGTATTTCTG      240
76 GGTATTCACC GTAAAAGAAA TTCCATTCAA ATTTATCTAC TTAACGTAGC CATTGCAGAC      300
78 CTCCTACTCA TCTTCTGCCT CCCTTTCCGA ATAATGTATC ATATTAACCA AAACAAGTGG      360
80 AACTAGGTG TGATTCTGTG CAAGGTTGTG GGAACACTGC TTTATATGAA CATGTACATT      420
82 AGCATTATTT TGCTTGGATT CATCAGTTTG GATCGCTATA TAAAAATTAA TCGGTCTATA      480
84 CAGCAACGGA AGGCAATAAC AACCACAAAG AGTATTTATG TCTGTTGTAT AGTATGGATG      540
86 CTGCTCTTGT GTGGATTCTT AACTATGATT ATTTTAAACAC TTAAGAAAGG AGGGCATAAT      600
88 TCCACAATGT GTTTCATTAT CAGAGATAAG CATAACGCAA AAGGAGAAGC CATTTTTAAAC      660
90 TTCATTCTTG TGGTAATGTT CTGGCTAATT TTCTTACTAA TAATCCTTTC ATATATTAAG      720
92 ATTGGAAGA ATCTATTGAG GATTTCTAAA AGGAGGTCAA AATTTCTTAA TTCTGGTAAA      780
94 TATGCCACTA CAGCTCGTAA CTCCTTTATT GTACTTATCA TTTTACTAT ATGTGTGGGT      840
96 CCCTATCATG CCTTTCGATT CATCTACATT TCTTCACAGC TAAATGTATC ATCTTGCTAC      900
98 TGGAAAGAAA TTGTTACAAA AACCAATGAG ATCATGCTGG TTCTCTCATC TTTCAATAGT      960
100 TGGTTAGATC CAGTCATGTA TTTCTGATG TCCAGTAACA TTCGCAAAAT AATGTGCCAA      1020
102 CTTCTTTTTT GACGATTTCA AGGTGAACCA AGTAGGAGTG AAAGCACTTC AGAATTTAAA      1080
104 CCAGGATACT CCCTGCATGA TACATCTGTG GCAGGGAAAA TACAGTCTAG TTCTGAAAGT      1140
106 ACT      1143
110 (2) INFORMATION FOR SEQ ID NO: 2:
112      (i) SEQUENCE CHARACTERISTICS:
113          (A) LENGTH: 381 amino acids
114          (B) TYPE: amino acid
115          (D) TOPOLOGY: linear
117      (ii) MOLECULE TYPE: protein
119      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
121 Met Arg Ser His Thr Ile Thr Met Thr Thr Thr Ser Val Ser Ser Trp
122 1 5 10 15
124 Pro Tyr Ser Ser His Arg Met Arg Phe Ile Thr Asn His Ser Asp Gln
125 20 25 30
127 Pro Pro Gln Asn Phe Ser Ala Thr Pro Asn Val Thr Thr Cys Pro Met
128 35 40 45
130 Asp Glu Lys Leu Leu Ser Thr Val Leu Thr Thr Ser Tyr Ser Val Ile
131 50 55 60
133 Phe Ile Val Gly Leu Val Gly Asn Ile Ile Ala Pro Tyr Val Phe Leu
134 65 70 75 80
136 Gly Ile His Arg Lys Arg Asn Ser Ile Gln Ile Tyr Leu Leu Asn Val
137 85 90 95
139 Ala Ile Ala Asp Leu Leu Leu Ile Phe Cys Leu Pro Phe Arg Ile Met
140 100 105 110
142 Tyr His Ile Asn Gln Asn Lys Trp Thr Leu Gly Val Ile Leu Cys Lys
143 115 120 125
145 Val Val Gly Thr Leu Leu Tyr Met Asn Met Tyr Ile Ser Ile Ile Leu
146 130 135 140
148 Leu Gly Phe Ile Ser Leu Asp Arg Tyr Ile Lys Ile Asn Arg Ser Ile
149 145 150 155 160

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151 Gln Gln Arg Lys Ala Ile Thr Thr Lys Gln Ser Ile Tyr Val Cys Cys
152          165          170          175
154 Ile Val Trp Met Leu Ala Leu Gly Gly Phe Leu Thr Met Ile Ile Leu
155          180          185          190
157 Thr Leu Lys Lys Gly Gly His Asn Ser Thr Met Cys Phe His Tyr Arg
158          195          200          205
160 Asp Lys His Asn Ala Lys Gly Glu Ala Ile Phe Asn Phe Ile Leu Val
161          210          215          220
163 Val Met Phe Trp Leu Ile Phe Leu Leu Ile Ile Leu Ser Tyr Ile Lys
164 225          230          235          240
166 Ile Gly Lys Asn Leu Leu Arg Ile Ser Lys Arg Arg Ser Lys Phe Pro
167          245          250          255
169 Asn Ser Gly Lys Tyr Ala Thr Thr Ala Arg Asn Ser Phe Ile Val Leu
170          260          265          270
172 Ile Ile Phe Thr Ile Cys Val Gly Pro Tyr His Ala Phe Arg Phe Ile
173          275          280          285
175 Tyr Ile Ser Ser Gln Leu Asn Val Ser Ser Cys Tyr Trp Lys Glu Ile
176          290          295          300
178 Val His Lys Thr Asn Glu Ile Met Leu Val Leu Ser Ser Phe Asn Ser
179 305          310          315          320
181 Trp Leu Asp Pro Val Met Tyr Phe Leu Met Ser Ser Asn Ile Arg Lys
182          325          330          335
184 Ile Met Cys Gln Leu Leu Phe Arg Arg Phe Gln Gly Glu Pro Ser Arg
185          340          345          350
187 Ser Glu Ser Thr Ser Glu Phe Lys Pro Gly Tyr Ser Leu His Asp Thr
188          355          360          365
191 Ser Val Ala Gly Lys Ile Gln Ser Ser Ser Glu Ser Thr
192          370          375          380

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VERIFICATION SUMMARY

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]